We claim:

1. A substantially purified nucleic acid molecule that encodes a maize, soybean or *Arabidopsis thaliana* transcription factor or fragment thereof, wherein said maize or soybean transcription factor is selected from the group consisting of:

(a) homeobox transcription factor;

(b) HLH transcription factor;

(c) leucine zipper transcription factor;

(d) zinc finger transcription factor; and

(e) other transcription factor.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 3853.

3. A substantially purified maize or soybean transcription factor or fragment thereof, wherein said maize, soybean or *Arabidopsis thaliana* transcription factor is selected from the group consisting of

(a) homeobox transcription factor or fragment thereof;

(b) HLH transcription factor or fragment thereof;

(c) leucine zipper transcription factor or fragment thereof;

(d) zinc finger transcription factor or fragment thereof and

(e) other transcription factor or fragment thereof.

4. A substantially purified maize, soybean or *Arabidopsis thaliana* transcription factor or fragment thereof according to claim 3, wherein said maize, soybean or *Arabidopsis thaliana*

transcription factor or fragment thereof is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of consisting of SEQ ID NO: 1 through SEQ ID NO: 3853.

5. A substantially purified antibody or fragment thereof which is capable of specifically binding to a specific maize, soybean or *Arabidopsis thaliana* transcription factor or fragment thereof according to claim 4.

6. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule;

(B) a structural nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

(a) a nucleic acid sequence which encodes for a homeobox transcription factor or fragment thereof;

(b) a nucleic acid sequence which encodes for a HLH transcription factor or fragment thereof;

(c) a nucleic acid sequence which encodes for a leucine zipper transcription factor or fragment thereof;

(d) a nucleic acid sequence which encodes for a zinc finger transcription factor or fragment thereof;

(e) a nucleic acid sequence which encodes for another transcription factor or fragment thereof;

(f) a nucleic acid sequence which is complementary to any of the nucleic acid sequences of (a) through (e); and

(C) a 3' non-translated sequence that functions in said plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

7. The transformed plant according to claim 6, wherein said structural gene is complementary to any of the nucleic acid sequences of (a) through (e).

8. A method for determining a level or pattern in a plant cell of an transcription factor in a plant metabolic pathway comprising:

(A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid molecule, said marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 3853 or compliments thereof, with a complementary nucleic acid molecule obtained from said plant cell or plant tissue, wherein nucleic acid hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue permits the detection of an mRNA for said transcription factor;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant cell or plant tissue; and

(C) detecting the level or pattern of said complementary nucleic acid, wherein the detection of said complementary nucleic acid is predictive of the level or pattern of said transcription factor in said plant metabolic pathway.

9. The method of claim 8, wherein said level or pattern is detected by *in situ* hybridization.